

(1) GENERAL INFORMATION:

(i) APPLICANTS: Goodearl, Andrew; Stroobant, Paul; Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark; Chen, Maio Su; Hiles, Ian

(ii) TITLE OF INVENTION: Glial Mitogenic Factors, Their Preparation and Use

(iii) NUMBER OF SEQUENCES: 184

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(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
(B) COMPUTER: IBM
(C) OPERATING SYSTEM: PC-DOS
(D) SOFTWARE: Wordperfect

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/036,555
(B) FILING DATE: 24-MAR-1993
(C) CLASSIFICATION: 530

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 07/965,173
(B) FILING DATE: 23-OCT-1992

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 07/940,389
(B) FILING DATE: 03-SEP-1992

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 07/907,138
(B) FILING DATE: 30-JUN-1992

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 07/863,703
(B) FILING DATE: 03-APRIL-1992

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: U.K. 91 07566.3
(B) FILING DATE: 10-APRIL-1991

(viii) ATTORNEY/AGENT INFORMATION:

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Phe Lys Gly Asp Ala His Thr Glu

1

5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine;
Xaa in position 12 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Xaa Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Xaa Lys

1

5

10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine;
Xaa in position 10 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Xaa Thr Glu Thr Ser Ser Ser Gly Leu Xaa Leu Lys

1

5

10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Xaa Lys Leu Gly Glu Met Trp Ala Glu
1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Xaa Leu Gly Glu Lys Arg Ala
1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Xaa Ile Lys Ser Glu His Ala Gly Leu Ser Ile Gly Asp Thr Ala Lys
1 5 10 15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Xaa Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Arg Lys
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Xaa Ile Lys Gly Glu His Pro Gly Leu Ser Ile Gly Asp Val Ala Lys
1 5 10 15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine
and Xaa in position 12 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Xaa Met Ser Glu Tyr Ala Phe Phe Val Gln Thr Xaa Arg
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Xaa Ser Glu His Pro Gly Leu Ser Ile Gly Asp Thr Ala Lys
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine;
Xaa in position 8 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Xaa Ala Gly Tyr Phe Ala Glu Xaa Ala Arg
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine;
Xaa in position 7 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Xaa Lys Leu Glu Phe Leu Xaa Ala Lys
1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Xaa Thr Thr Glu Met Ala Ser Glu Gln Gly Ala
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Xaa Ala Lys Glu Ala Leu Ala Ala Leu Lys
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Xaa Phe Val Leu Gln Ala Lys Lys
1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Xaa Leu Gly Glu Met Trp
1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Glu Tyr Lys Cys Leu Lys Phe Lys Trp Phe Lys Lys Ala Thr Val Met
1 5 10 15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 8 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Glu Ala Lys Tyr Phe Ser Lys Xaa Asp Ala
1 5 10

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 19:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ix) FEATURE:
- (D) OTHER INFORMATION: Xaa in position 2 is unknown.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Glu Xaa Lys Phe Tyr Val Pro
 1 5

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 20:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Glu Leu Ser Phe Ala Ser Val Arg Leu Pro Gly Cys Pro Pro Gly Val
 1 5 10 15

Asp Pro Met Val Ser Phe Pro Val Ala Leu
 20 25

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 21:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2003
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ix) FEATURE:
- (D) OTHER INFORMATION: N in positions 31 and 32 could be either A or G.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GGAATTCCTT	TTTTTTTTTT	TTTTTTTCTT	NNTTTTTTTT	TGCCCTTATA	CCTCTTCGCC	60
TTTCTGTGGT	TCCATCCACT	TCTTCCCCCT	CCTCCTCCCA	TAAACAACCTC	TCCTACCCCT	120
GCACCCCAA	TAAATAAATA	AAAGGAGGAG	GGCAAGGGGG	GAGGAGGAGG	AGTGGTGCTG	180
CGAGGGGAAG	GAAAAGGGAG	GCAGCGCGAG	AAGAGCCGGG	CAGAGTCCGA	ACCGACAGCC	240
AGAAGCCCGC	ACGCACCTCG	CACC ATG AGA	TGG CGA CGC	GCC CCG CGC	CGC CGC	291
		Met Arg Trp Arg	Arg Ala Pro	Arg Arg		
		1	5			

TCC Ser 10	GGG Gly	CGT Arg	CCC Pro	GGC Gly 15	CCC Pro	CGG Arg	GCC Ala	CAG Gln	CGC Arg 20	CCC Pro	GGC Gly	TCC Ser	GCC Ala	GCC Ala	CGC Arg 25	339
TCG Ser	TCG Ser	CCG Pro	CCG Pro	CTG Leu 30	CCG Pro	CTG Leu	CTG Leu	CCA Pro	CTA Leu 35	CTG Leu	CTG Leu	CTG Leu	CTG Leu	GGG Gly 40	ACC Thr	387
GCG Ala	GCC Ala	CTG Leu 45	GCG Ala	CCG Pro	GGG Gly	GCG Ala	GCG Ala	GCC Ala	GGC Gly 50	AAC Asn	GAG Glu	GCG Ala	GCT Ala 55	CCC Pro	GCG Ala	435
GGG Gly	GCC Ala	TCG Ser 60	GTG Val	TGC Cys	TAC Tyr	TCG Ser	TCC Ser 65	CCG Pro	CCC Pro	AGC Ser	GTG Val	GGA Gly 70	TCG Ser	GTG Val	CAG Gln	483
GAG Glu 75	CTA Leu	GCT Ala	CAG Gln	CGC Arg	GCC Ala	GCG Ala	GTG Val 80	GTG Val	ATC Ile	GAG Glu	GGA Gly 85	AAG Lys	GTG Val	CAC His	CCG Pro	531
CAG Gln 90	CGG Arg	CGG Arg	CAG Gln	CAG Gln	GGG Gly 95	GCA Ala	CTC Leu	GAC Asp	AGG Arg	AAG Lys 100	GCG Ala	GCG Ala	GCG Ala	GCG Ala	GCG Ala 105	579
GGC Gly	GAG Glu	GCA Ala	GGG Gly 110	GCG Ala	TGG Trp	GGC Gly	GGC Gly	GAT Asp	CGC Arg 115	GAG Glu	CCG Pro	CCA Pro	GCC Ala	GCG Ala	GGC Gly 120	627
CCA Pro	CGG Arg	GCG Ala	CTG Leu 125	GGG Gly	CCG Pro	CCC Pro	GCC Ala	GAG Glu 130	GAG Glu	CCG Pro	CTG Leu	CTC Leu	GCC Ala 135	GCC Ala	AAC Asn	675
GGG Gly	ACC Thr 140	GTG Val	CCC Pro	TCT Ser	TGG Trp	CCC Pro	ACC Thr 145	GCC Ala	CCG Pro	GTG Val	CCC Pro	AGC Ser 150	GCC Ala	GGC Gly	GAG Glu	723
CCC Pro 155	GGG Gly	GAG Glu	GAG Glu	GCG Ala	CCC Pro	TAT Tyr 160	CTG Leu	GTG Val	AAG Lys	GTG Val	CAC His 165	CAG Gln	GTG Val	TGG Trp	GCG Ala	771
GTG Val 170	AAA Lys	GCC Ala	GGG Gly	GGC Gly	TTG Leu 175	AAG Lys	AAG Lys	GAC Asp	TCG Ser	CTG Leu 180	CTC Leu	ACC Thr	GTG Val	CGC Arg	CTG Leu 185	819
GGG Gly	ACC Thr	TGG Trp	GGC Gly	CAC His 190	CCC Pro	GCC Ala	TTC Phe	CCC Pro	TCC Ser 195	TGC Cys	GGG Gly	AGG Arg	CTC Leu	AAG Lys 200	GAG Glu	867
GAC Asp	AGC Ser	AGG Arg	TAC Tyr 205	ATC Ile	TTC Phe	TTC Phe	ATG Met	GAG Glu 210	CCC Pro	GAC Asp	GCC Ala	AAC Asn	AGC Ser 215	ACC Thr	AGC Ser	915

[illegible]

TTAACAAAAG	CAATTGTATT	ACTTCCTCTG	TTCGCGACTA	GTTGGCTCTG	AGATACTAAT	1710
AGGTGTGTGA	GGCTCCGGAT	GTTTCTGGAA	TTGATATTGA	ATGATGTGAT	ACAAATTGAT	1770
AGTCAATATC	AAGCAGTGAA	ATATGATAAT	AAAGGCATTT	CAAAGTCTCA	CTTTTATTGA	1830
TAAAATAAAA	ATCATTCTAC	TGAACAGTCC	ATCTTCTTTA	TACAATGACC	ACATCCTGAA	1890
AAGGGTGTTG	CTAAGCTGTA	ACCGATATGC	ACTTGAAATG	ATGGTAAGTT	AATTTTGATT	1950
CAGAATGTGT	TATTTGTCAC	AAATAAACAT	AATAAAAGGA	AAAAAAAAAA	AAA	2003

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 22:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 11 is unknown.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Xaa Lys
 1 5 10

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 23:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 9 is unknown.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Thr Glu Thr Ser Ser Ser Gly Leu Xaa Leu Lys
 1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Arg Lys
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 7 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Ala Gly Tyr Phe Ala Glu Xaa Ala Arg
1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Thr Thr Glu Met Ala Ser Glu Gln Gly Ala
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Ala Lys Glu Ala Leu Ala Ala Leu Lys
1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Phe Val Leu Gln Ala Lys Lys
1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Glu Thr Gln Pro Asp Pro Gly Gln Ile Leu Lys Lys Val Pro Met Val
1 5 10 15

Ile Gly Ala Tyr Thr
20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in positions 1, 3, 17 and 19 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Xaa Glu Xaa Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Glu
1 5 10 15
Xaa Gly Xaa Gly Lys
20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in position 6 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Lys Leu Glu Phe Leu Xaa Ala Lys
1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Xaa Val His Gln Val Trp Ala Ala Lys
1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine,
Xaa in position 11 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Xaa Tyr Ile Phe Phe Met Glu Pro Glu Ala Xaa Ser Ser Gly
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine,
Xaa in position 13 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Xaa Leu Gly Ala Trp Gly Pro Pro Ala Phe Pro Val Xaa Tyr
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Xaa Trp Phe Val Val Ile Glu Gly Lys
1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

Xaa Ala Ser Pro Val Ser Val Gly Ser Val Gln Glu Leu Val Gln Arg
1 5 10 15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Xaa Val Cys Leu Leu Thr Val Ala Ala Leu Pro Pro Thr
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 39:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ix) FEATURE:
 (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine;
 Xaa in position 6 is unknown.
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

Xaa Asp Leu Leu Leu Xaa Val
 1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 40:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Cys Thr Cys Gly Cys Cys Lys Cys Cys Arg Thr Thr Cys Ala Cys Arg
 1 5 10 15
 Cys Ala Gly Ala Ala Gly Gly Thr Cys Thr Thr Cys Thr Cys Cys Thr
 20 25 30
 Thr Cys Thr Cys Ala Gly Cys
 35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 41:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

Cys Cys Thr Cys Gly Cys Thr Cys Cys Thr Thr Cys Thr Thr Cys Thr
 1 5 10 15
 Thr Gly Cys Cys Cys Thr Thr Cys
 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

AAGTGCCCAA ATGAGTTTAC TGGTGATCGC TGCCAAAACT ACGTAATGGC CAGCTTCTAC

60

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

AGTACGTCCA CTCCCTTTCT GTCTCTGCCT GAATAG

36

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

AAGGCGGAGG	AGCTGTACCA	GAAGAGAGTG	CTGACCATAA	CCGGCATCTG	CATCGCCCTC	60
CTTGTGGTCG	GCATCATGTG	TGTGGTGGCC	TACTGCAAAA	CCAAGAAACA	GCGGAAAAAG	120
CTGCATGACC	GTCTTCGGCA	GAGCCTTCGG	TCTGAACGAA	ACAATATGAT	GAACATTGCC	180
AATGGGCCTC	ACCATCCTAA	CCCACCCCCC	GAGAATGTCC	AGCTGGTGAA	TCAATACGTA	240
TCTAAAAACG	TCATCTCCAG	TGAGCATATT	GTTGAGAGAG	AAGCAGAGAC	ATCCTTTTCC	300
ACCAGTCACT	ATACTTCCAC	AGCCCATCAC	TCCACTACTG	TCACCCAGAC	TCCTAGCCAC	360
AGCTGGAGCA	ACGGACACAC	TGAAAGCATC	CTTTCCGAAA	GCCACTCTGT	AATCGTGATG	420
TCATCCGTAG	AAAACAGTAG	GCACAGCAGC	CCAAGTGGGG	GCCCAAGAGG	ACGTCTTAAT	480
GGCACAGGAG	GCCCTCGTGA	ATGTAACAGC	TTCCTCAGGC	ATGCCAGAGA	AACCCCTGAT	540
TCCTACCGAG	ACTCTCCTCA	TAGTGAAAG				569

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

Val His Gln Val Trp Ala Ala Lys
1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 10 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Tyr Ile Phe Phe Met Glu Pro Glu Ala Xaa Ser Ser Gly
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 12 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

Leu Gly Ala Trp Gly Pro Pro Ala Phe Pro Val Xaa Tyr
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Trp Phe Val Val Ile Glu Gly Lys
1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

Ala Ser Pro Val Ser Val Gly Ser Val Gln Glu Leu Val Gln Arg
1 5 10 15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Val Cys Leu Leu Thr Val Ala Ala Leu Pro Pro Thr
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Lys Val His Gln Val Trp Ala Ala Lys
1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 12 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Xaa Lys
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 5 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Asp Leu Leu Leu Xaa Val
1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

TTYAARGGNG AYGNCAYAC 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

CATRTAYTCR TAYTCRTCNG C 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

TGYTCNGANG CCATYTCNGT 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

TGYTCRCTNG CCATYTCNGT 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

CCDATNACCA TNGGNACYTT 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GCNGCCCAN A CYTGRTGNAC 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

GCYTCNGGYT CCATRAARAA 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 61:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

CCYTCDATNA CNACRAACCA 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 62:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

TCNGCRAART ANCCNGC 17

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 63:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

GCNGCNAGNG CYTCYTTNGC 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 64:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GCNGCYAANG CYTCYTTNGC 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 65:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

TTYTTNGCYT GNAGNACRAA 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 66:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

TTYTTNGCYT GYAANACRAA 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 67:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

TGNACNAGYT CYTGNAC 17

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 68:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

TGNACYAAYT CYTGNAC 17

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 69:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

CATRTAYTCN CCNGARTCNG C 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 70:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

CATRTAYTCN CCRCTRTCNG C 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 71:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

NGARTCNGCY AANGANGCYT T 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 72:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

NGARTCNGCN AGNGANGCYT T 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

RCTRTCNGCY AANGANGCYT T 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

RCTRTCNGCN AGNGANGCYT T 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

NGARTCNGCY AARCTNGCYT T 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

NGARTCNGCN AGRCTNGCYT T 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 730
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GTATGTGTCA	GCCATGACCA	CCCCGGCTCG	TATGTCACCT	GTAGATTTCC	ACACGCCAAG	60
CTCCCCCAA	TCGCCCCCTT	CGGAAATGTC	TCCACCCGTG	TCCAGCATGA	CGGTGTCCAT	120
GCCTTCCATG	GCGGTCAGCC	CCTTCATGGA	AGAAGAGAGA	CCTCTACTTC	TCGTGACACC	180
ACCAAGGCTG	CGGGAGAAGA	AGTTTGACCA	TCACCCTCAG	CAGTTCAGCT	CCTTCCACCA	240
CAACCCCGCG	CATGACAGTA	ACAGCCTCCC	TGCTAGCCCC	TTGAGGATAG	TGGAGGATGA	300
GGAGTATGAA	ACGACCCAAG	AGTACGAGCC	AGCCCAAGAG	CCTGTTAAGA	AACTCGCCAA	360
TAGCCGGCGG	GCCAAAAGAA	CCAAGCCCAA	TGGCCACATT	GCTAACAGAT	TGGAAGTGGA	420
CAGCAACACA	AGCTCCCAGA	GCAGTAACTC	AGAGAGTGAA	ACAGAAGATG	AAAGAGTAGG	480
TGAAGATACG	CCTTTCCTGG	GCATACAGAA	CCCCCTGGCA	GCCAGTCTTG	AGGCAACACC	540
TGCCTTCCGC	CTGGCTGACA	GCAGGACTAA	CCCAGCAGGC	CGCTTCTCGA	CACAGGAAGA	600
AATCCAGGCC	AGGCTGTCTA	GTGTAATTGC	TAACCAAGAC	CCTATTGCTG	TATAAAACCT	660
AAATAAACAC	ATAGATTCAC	CTGTAAAACT	TTATTTTATA	TAATAAAGTA	TTCCACCTTA	720
AATTAAACAA						730

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

RCTRTCNGCY AARCTNGCYT T 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

RCTRCTNGCN AGRCTNGCYT T 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

ACNACNGARA TGGCTCNNGA 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

ACNACNGARA TGGCAGYNGA 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 82:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

CAYCARGTNT GGGCNGCNAA 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 83:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

TTYGTNGTNA THGARGGNAA 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 84:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

AARGGNGAYG CNCAYACNGA 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 85:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

GARGCNYTNG CNGCNYTNAA 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 86:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

GTNCGNTCNG TNCARGARYT 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 87:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

GTNCGNAGYG TNCARGARYT 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 88:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

NACYTTYTTN ARDATYTGNC C 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in positions 14, 23, 90, 100, 126, and 135 is a stop codon.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

TCTAA AAC TAC AGA GAC TGT ATT TTC ATG ATC ATC ATA GTT CTG TGA AAT ATA	53
Asn Tyr Arg Asp Cys Ile Phe Met Ile Ile Ile Val Leu Xaa Asn Ile	
1 5 10 15	
CTT AAA CCG CTT TGG TCC TGA TCT TGT AGG AAG TCA GAA CTT CGC ATT	101
Leu Lys Pro Leu Trp Ser Xaa Ser Cys Arg Lys Ser Glu Leu Arg Ile	
20 25 30	
AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC	149
Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Ser Met Cys Lys Val Ile	
35 40 45	
AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG	197
Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Arg Ile Val Glu	
50 55 60	
TCA AAC GGT AAG AGA TGC CTA CTG CGT GCT ATT TCT CAG TCT CTA AGA	245
Ser Asn Gly Lys Arg Cys Leu Leu Arg Ala Ile Ser Gln Ser Leu Arg	
65 70 75 80	
GGA GTG ATC AAG GTA TGT GGT CAC ACT TGA ATC ACG CAG GTG TGT GAA	293
Gly Val Ile Lys Val Cys Gly His Thr Xaa Ile Thr Gln Val Cys Glu	
85 90 95	
ATC TCA TTG TGA ACA AAT AAA AAT CAT GAA AGG AAA ACT CTA TGT TTG	341
Ile Ser Cys Xaa Thr Asn Lys Asn His Glu Arg Lys Thr Leu Cys Leu	
100 105 110	
AAA TAT CTT ATG GGT CCT CCT GTA AAG CTC TTC ACT CCA TAA GGT GAA	389
Lys Tyr Leu Met Gly Pro Pro Val Lys Leu Phe Thr Pro Xaa Gly Glu	
115 120 125	
ATA GAC CTG AAA TAT ATA TAG ATT ATT T	417
Ile Asp Leu Lys Tyr Ile Xaa Ile Ile	
130 135	

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 90:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ix) FEATURE:
 (D) OTHER INFORMATION: N at positions 19, 25, and 31 is Inosine.
 Y can be cytidine or thymidine.
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

CCGAATTCTG CAGGARACNC ARCCNGAYCC NGG 33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 91:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ix) FEATURE:
 (D) OTHER INFORMATION: N at positions 14, 20, 23, 29, and 35 is
 Inosine.
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

AAGGATCCTG CAGNGTRTAN GCNCCDATNA CCATNGG 37

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 92:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ix) FEATURE:
 (D) OTHER INFORMATION: N at positions 16, 21, and 24 is Inosine.
 Y can be cytidine or thymidine.
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

CCGAATTCTG CAGGCNGAYT CNGGNGARTA YATG 34

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at positions 16 and 25 is Inosine. Y
can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

CCGAATTCTG CAGGCNGAYA GYGGNGARTA YAT 33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at positions 14, 15, 16, 26, and 29 is
Inosine. Y can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

AAGGATCCTG CAGNNNCATR TAYTCNCCNG ARTC 34

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at positions 14, 15, 16, and 26 is
Inosine. Y can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

AAGGATCCTG CAGNNNCATR TAYTCNCCRC TRTC 34

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at positions 21, 28, and 31 is Inosine.
Y can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

CCGAATTCTG CAGCAYCARG TNTGGGCNGC NAA 33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at position 31 is Inosine. Y can be
cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

CCGAATTCTG CAGATHTTYT TYATGGARCC NGARG 35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at positions 18, 21, 24, 27, and 33 is
Inosine. Y can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

CCGAATTCTG CAGGGGGNCC NCCNGCNTTY CCNGT 35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at positions 21 and 24 is Inosine. Y
can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

CCGAATTCTG CAGTGGTTYG TNGTNATHGA RGG 33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at positions 17, 20, and 26 is Inosine.
Y can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

AAGGATCCTG CAGYTTNGCU NGCCCANACY TGRTG 35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at position 19 is Inosine. Y can be
cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

AAGGATCCTG CAGGCYTCNG GYTCCATRAA RAA 33

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 102:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: N at positions 16, 22, 25, 28, and 31 is Inosine.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

AAGGATCCTG CAGACNGGRA ANGCNNGNGG NCC 33

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 103:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: N at positions 17, 26, and 29 is Inosine. Y can be cytidine or thymidine.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

AAGGATCCTG CAGYTTNCCY TCDATNACNA CRAAC 35

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 104:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: N at position 18 is Inosine. Y can be cytidine or thymidine.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

CATRTAYTCR TAYTCTCNGC AAGGATCCTG CAG 33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at position 19, 25, and 31 is Inosine.
Y can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

CCGAATTCTG CAGAARGGNG AYGNCAYAC NGA 33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at position 3 and 18 is Inosine. Y can
be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

GCNGCYAANG CYTCYTNGC AAGATCCTG CAG 33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at position 3, 6, 9, and 18 is Inosine.
Y can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

GCNGCNAGNG CYTCYTNGC AAGATCCTG CAG 33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at position 3, 12, and 15 is Inosine. Y
can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

TCNGCRAART ANCCNGCAAG GATCCTGCAG 30

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

CATCGATCTG CAGGCTGATT CTGGAGAATA TATGTGCA 38

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

AAGGATCCTG CAGCCACATC TCGAGTCGAC ATCGATT 37

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 111:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

CCGAATTCTG CAGTGATCAG CAAACTAGGA AATGACA 37

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 112:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

CATCGATCTG CAGCCTAGTT TGCTGATCAC TTTGCAC 37

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 113:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

AAGGATCCTG CAGTATATTC TCCAGAATCA GCCAGTG 37

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 114:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

AAGGATCCTG CAGGCACGCA GTAGGCATCT CTTA 34

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 115:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

CCGAATTCTG CAGCAGAACT TCGCATTAGC AAAGC 35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 116:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

CATCCCGGGA TGAAGAGTCA GGAGTCTGTG GCA 33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 117:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

ATACCCGGGC TGCAGACAAT GAGATTTAC ACACCTGCG 39

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 118:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

AAGGATCCTG CAGTTTGGA CCTGCCACAG ACTCCT 36

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

ATACCCGGGC TGCAGATGAG ATTCACACA CCTGCGTGA 39

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

His Gln Val Trp Ala Ala Lys Ala Ala Gly Leu Lys
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

Gly Gly Leu Lys Lys Asp Ser Leu Leu Thr Val Arg Leu Gly Ala Asn
1 5 10 15

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 122:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 12 is unknown.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

Leu Gly Ala Trp Gly Pro Pro Ala Phe Pro Val Xaa Tyr
 1 5 10

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 123:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

Leu Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser
 1 5 10 15

Cys Gly Arg Leu Lys Glu Asp
 20

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 124:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 10 is unknown.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

Tyr Ile Phe Phe Met Glu Pro Glu Ala Xaa Ser Ser Gly
 1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu Ala Asn Ser
1 5 10 15

Ser Gly Gly Pro Gly Arg Leu
20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

Glu Tyr Lys Cys Leu Lys Phe Lys Trp Phe Lys Lys Ala Thr Val Met
1 5 10 15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys
1 5 10 15

Asn Gly Ser Glu Leu Ser Arg Lys Asn Lys
20 25

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 12 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Xaa Lys
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met
1 5 10 15

Cys Lys Val Ile Ser Lys Leu
20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Arg Lys
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys
1 5 10 15

Lys Val Ile Ser Lys Leu
20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 744
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

CCTGCAG CAT CAA GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG 55
His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu
1 5 10 15

CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC TGC 103
Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys
20 25 30

GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG 151
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu
35 40 45

GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC CCC	199
Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro	
50 55 60	
TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG	247
Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val	
65 70 75 80	
CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG	295
Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu	
85 90 95	
TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA	343
Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu	
100 105 110	
TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC	391
Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser	
115 120 125	
CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG	439
Arg Lys Asn Lys Pro Glu Asn Ile Lys Ile Gln Lys Arg Pro Gly Lys	
130 135 140	
TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT	487
Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr	
145 150 155 160	
ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC	535
Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn	
165 170 175	
ATC ACC ATT GTG GAG TCA AAC GGT AAG AGA TGC CTA CTG CGT GCT ATT	583
Ile Thr Ile Val Glu Ser Asn Gly Lys Arg Cys Leu Leu Arg Ala Ile	
180 185 190	
TCT CAG TCT CTA AGA GGA GTG ATC AAG GTA TGT GGT CAC ACT	625
Ser Gln Ser Leu Arg Gly Val Ile Lys Val Cys Gly His Thr	
195 200 205	
TGAATCACGC AGGTGTGTGA AATCTCATTG TGAACAAATA AAAATCATGA AAGGAAAAAA	685
AAAAAAAAAA AATCGATGTC GACTCGAGAT GTGGCTGCAG GTCGACTCTA GAGGATCCC	744

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1193
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

CCTGCAG	CAT	CAA	GTG	TGG	GCG	GCG	AAA	GCC	GGG	GGC	TTG	AAG	AAG	GAC	TCG	CTG	55
	His	Gln	Val	Trp	Ala	Ala	Lys	Ala	Gly	Gly	Leu	Lys	Lys	Asp	Ser	Leu	
	1				5					10					15		
CTC	ACC	GTG	CGC	CTG	GGC	GCC	TGG	GGC	CAC	CCC	GCC	TTC	CCC	TCC	TGC		103
Leu	Thr	Val	Arg	Leu	Gly	Ala	Trp	Gly	His	Pro	Ala	Phe	Pro	Ser	Cys		
			20					25					30				
GGG	CGC	CTC	AAG	GAG	GAC	AGC	AGG	TAC	ATC	TTC	TTC	ATG	GAG	CCC	GAG		151
Gly	Arg	Leu	Lys	Glu	Asp	Ser	Arg	Tyr	Ile	Phe	Phe	Met	Glu	Pro	Glu		
		35					40					45					
GCC	AAC	AGC	AGC	GGC	GGG	CCC	GGC	CGC	CTT	CCG	AGC	CTC	CTT	CCC	CCC		199
Ala	Lys	Ser	Ser	Gly	Gly	Pro	Gly	Arg	Leu	Pro	Ser	Leu	Leu	Pro	Pro		
	50					55					60						
TCT	CGA	GAC	GGG	CCG	GAA	CCT	CAA	GAA	GGA	GGT	CAG	CCG	GGT	GCT	GTG		247
Ser	Arg	Asp	Gly	Pro	Glu	Pro	Gln	Glu	Gly	Gly	Gln	Pro	Gly	Ala	Val		
65					70				75						80		
CAA	CGG	TGC	GCC	TTG	CCT	CCC	CGC	TTG	AAA	GAG	ATG	AAG	AGT	CAG	GAG		295
Gln	Arg	Cys	Ala	Leu	Pro	Pro	Arg	Leu	Lys	Glu	Met	Lys	Ser	Gln	Glu		
				85					90					95			
TCT	GTG	GCA	GGT	TCC	AAA	CTA	GTG	CTT	CGG	TGC	GAG	ACC	AGT	TCT	GAA		343
Ser	Val	Ala	Gly	Ser	Lys	Leu	Val	Leu	Arg	Cys	Glu	Thr	Ser	Ser	Glu		
			100					105					110				
TAC	TCC	TCT	CTC	AAG	TTC	AAG	TGG	TTC	AAG	AAT	GGG	AGT	GAA	TTA	AGC		391
Tyr	Ser	Ser	Leu	Lys	Phe	Lys	Trp	Phe	Lys	Asn	Gly	Ser	Glu	Leu	Ser		
			115				120					125					
CGA	AAG	AAC	AAA	CCA	GAA	AAC	ATC	AAG	ATA	CAG	AAA	AGG	CCG	GGG	AAG		439
Arg	Lys	Asn	Lys	Gly	Gly	Asn	Ile	Lys	Ile	Gln	Lys	Arg	Pro	Gly	Lys		
	130					135					140						
TCA	GAA	CTT	CGC	ATT	AGC	AAA	GCG	TCA	CTG	GCT	GAT	TCT	GGA	GAA	TAT		487
Ser	Glu	Leu	Arg	Ile	Ser	Lys	Ala	Ser	Leu	Ala	Asp	Ser	Gly	Glu	Tyr		
145					150				155						160		
ATG	TGC	AAA	GTG	ATC	AGC	AAA	CTA	GGA	AAT	GAC	AGT	GCC	TCT	GCC	AAC		535
Met	Cys	Lys	Val	Ile	Ser	Lys	Leu	Gly	Asn	Asp	Ser	Ala	Ser	Ala	Asn		
				165				170						175			

ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG ACA	583
Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly Thr	
180 185 190	
AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT	631
Ser His Leu Val Lys Ser Ala Glu Lys Glu Lys Thr Phe Cys Val Asn	
195 200 205	
GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC	679
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr	
210 215 220	
TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT	727
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn	
225 230 235 240	
GTG CCC ATG AAA GTC CAA ACC CAA GAA AGT GCC CAA ATG AGT TTA CTG	775
Val Pro Met Lys Val Gln Thr Gln Glu Ser Ala Gln Met Ser Leu Leu	
245 250 255	
GTG ATC GCT GCC AAA ACT ACG TAATGGCCAG CTTCTACAGT ACGTCCACTC	826
Val Ile Ala Ala Lys Thr Thr	
260	
CCTTTCTGTC TCTGCCTGAA TAGCGCATCT CAGTCGGTGC CGCTTTCTTG TTGCCGCATC	886
TCCCCTCAGA TTCCTCCTAG AGCTAGATGC GTTTTACCAG GTCTAACATT GACTGCCTCT	946
GCCTGTCGCA TGAGAACATT AACACAAGCG ATTGTATGAC TTCCTCTGTC CGTGACTAGT	1006
GGGCTCTGAG CTACTCGTAG GTGCGTAAGG CTCCAGTGTT TCTGAAATTG ATCTTGAATT	1066
ACTGTGATAC GACATGATAG TCCCTCTCAC CCAGTGCAAT GACAATAAAG GCCTTGAAAA	1126
GTCAAAAAAA AAAAAAATAA AAAAAATCGA TGTCGACTCG AGATGTGGCT GCAGGTCGAC	1186
TCTAGAG	1193

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1108
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

CCTGCAG CAT CAA GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG	55
His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu	
1 5 10 15	
CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC TGC	103
Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys	
20 25 30	
GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG	151
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu	
35 40 45	

GCC Ala	AAC Asn	AGC Ser	AGC Ser	GGC Gly	GGG Gly	CCC Pro	GGC Gly	CGC Arg	CTT Leu	CCG Pro	AGC Ser	CTC Leu	CTT Leu	CCC Pro	CCC Pro	199
50						55					60					
TCT Ser	CGA Arg	GAC Asp	GGG Gly	CCG Pro	GAA Glu	CCT Pro	CAA Gln	GAA Glu	GGA Gly	GGT Gly	CAG Gln	CCG Pro	GGT Gly	GCT Ala	GTG Val	247
65					70					75					80	
CAA Gln	CGG Arg	TGC Cys	GCC Ala	TTG Leu	CCT Pro	CCC Pro	CGC Arg	TTG Leu	AAA Lys	GAG Glu	ATG Met	AAG Lys	AGT Ser	CAG Gln	GAG Glu	295
			85						90					95		
TCT Ser	GTG Val	GCA Ala	GGT Gly	TCC Ser	AAA Lys	CTA Leu	GTG Val	CTT Leu	CGG Arg	TGC Cys	GAG Glu	ACC Thr	AGT Ser	TCT Ser	GAA Glu	343
			100				105					110				
TAC Tyr	TCC Ser	TCT Ser	CTC Leu	AAG Lys	TTC Phe	AAG Lys	TGG Trp	TTC Phe	AAG Lys	AAT Asn	GGG Gly	AGT Ser	GAA Glu	TTA Leu	AGC Ser	391
		115					120					125				
CGA Arg	AAG Lys	AAC Asn	AAA Lys	CCA Pro	GAA Glu	AAC Asn	ATC Ile	AAG Lys	ATA Ile	CAG Gln	AAA Lys	AGG Arg	CCG Pro	GGG Pro	AAG Lys	439
	130					135					140					
TCA Ser	GAA Glu	CTT Leu	CGC Arg	ATT Ile	AGC Ser	AAA Lys	GCG Ala	TCA Ser	CTG Leu	GCT Ala	GAT Asp	TCT Ser	GGA Gly	GAA Glu	TAT Tyr	487
145					150					155					160	
ATG Met	TGC Cys	AAA Lys	GTG Val	ATC Ile	AGC Ser	AAA Lys	CTA Leu	GGA Gly	AAT Asn	GAC Asp	AGT Ser	GCC Ala	TCT Ser	GCC Ala	AAC Asn	535
			165						170					175		
ATC Ile	ACC Arg	ATT Ile	GTG Val	GAG Glu	TCA Ser	AAC Asn	GCC Ala	ACA Thr	TCC Ser	ACA Thr	TCT Ser	ACA Thr	GCT Ala	GGG Gly	ACA Thr	583
			180					185					190			
AGC Ser	CAT His	CTT Leu	GTC Val	AAG Lys	TGT Cys	GCA Ala	GAG Glu	AAG Lys	GAG Glu	AAA Lys	ACT Thr	TTC Phe	TGT Cys	GTG Val	AAT Asn	631
		195					200					205				
GGA Gly	GGC Gly	GAG Glu	TGC Cys	TTC Phe	ATG Met	GTG Val	AAA Lys	GAC Asp	CTT Leu	TCA Ser	AAT Asn	CCC Pro	TCA Ser	AGA Arg	TAC Tyr	679
	210					215					220					
TTG Leu	TGC Cys	AAG Lys	TGC Cys	CCA Pro	AAT Asn	GAG Glu	TTT Phe	ACT Thr	GGT Gly	GAT Asp	CGC Arg	TGC Cys	CAA Gln	AAC Asn	TAC Tyr	727
225					230					235					240	
GTA Val	ATG Met	GCC Ala	AGC Ser	TTC Phe	TAC Tyr	AGT Ser	ACG Thr	TCC Ser	ACT Thr	CCC Pro	TTT Phe	CTG Leu	TCT Ser	CTG Leu	CCT Pro	775
				245					250					255		

GAA TAGCGCATCT CAGTCGGTGC CGCTTTCTTG TTGCCGCATC TCCCCTCAGA TTCCGCCTAG 838
Glu

AGCTAGATGC GTTTTACCAG GTCTAACATT GACTGCCTCT GCCTGTCGCA TGAGAACATT 898
AACACAAGCG ATTGTATGAC TTCCTCTGTC CGTGACTAGT GGGCTCTGAG CTACTCGTAG 958
GTGCGTAAGG CTCCAGTGTT TCTGAAATTG ATCTTGAATT ACTGTGATAC GACATGATAG 1018
TCCCTCTCAC CCAGTGCAAT GACAATAAAG GCCTTGAAAA GTCAAAAAAA AAAAAAAAAA 1078
AAAAATCGAT GTCGACTCGA GATGTGGCTG 1108

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N in position 214 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

AGTTTCCCCC CCCAACTTGT CGGAACTCTG GGCTCGCGCG CAGGGCAGGA GCGGAGCGGC 60
GGCGGCTGCC CAGGCGATGC GAGCGCGGGC CGGACGGTAA TCGCCTCTCC CTCCTCGGGC 120
TGCGAGCGCG CCGGACCGAG GCAGCGACAG GAGCGGACCG CGGCGGGAAC CGAGGACTCC 180
CCAGCGGCGC GCCAGCAGGA GCCACCCCGC GAGNCGTGCG ACCGGGACGG AGCGCCCGCC 240
AGTCCCAGGT GGCCCGGACC GCACGTTGCG TCCCCGCGCT CCCCGCCGGC GACAGGAGAC 300
GCTCCCCCCC ACGCCGCGCG CGCCTCGGCC CGGTCGCTGG CCCGCCTCCA CTCCGGGGAC 360
AAACTTTTCC CGAAGCCGAT CCCAGCCCTC GGACCCAAAC TTGTCGCGCG TCGCCTTCGC 420
CGGGAGCCGT CCGCGCAGAG CGTGCACTTC TCGGGCGAG ATG TCG GAG CGC AGA 474
Met Ser Glu Arg Arg
1 5

GAA GGC AAA GGC AAG GGG AAG GGC GGC AAG AAG GAC CGA GGC TCC GGC 522
Glu Gly Lys Gly Lys Gly Lys Gly Gly Lys Lys Asp Arg Gly Ser Gly
10 15 20

AAG AAG CCC GTG CCC GCG GCT GGC GGC CCG AGC CCA G 559
Lys Lys Pro Val Pro Ala Ala Gly Gly Pro Ser Pro Ala
25 30

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: N in position 8 could be either A or G.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

CC CAT CAN GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG	47
His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser	
1 5 10 15	
CTG CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC	95
Leu Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser	
20 25 30	
TGC GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC	143
Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro	
35 40 45	
GAG GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC	191
Glu Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro	
50 55 60	
CCC TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT	239
Pro Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala	
65 70 75	
GTG CAA CGG TGC G	252
Val Gln Arg Cys	
80	

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

CCT TGC CTC CCC GCT TGA AAG AGA TGA AGA GTC AGG AGT CTG TGG CAG	48
Leu Pro Pro Arg Leu Lys Glu His Lys Ser Gln Glu Ser Val Ala Gly	
1 5 10 15	
GTT CCA AAC TAG TGC TTC GGT GCG AGA CCA GTT CTG AAT ACT CCT CTC	96
Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu	
20 25 30	
TCA AGT TCA AGT GGT TCA AGA ATG GGA GTG AAT TAA GCC GAA AGA ACA	144
Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser Arg Lys Asn Lys	
35 40 45	
AAC CAC AAA ACA TCA AGA TAC AGA AAA GGC CGG G	178
Pro Gly Asn Ile Lys Ile Gln Lys Arg Pro Gly	
50 55	

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

G AAG TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA	46
Lys Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly	
1 5 10 15	
GAA TAT ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT	94
Glu Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser	
20 25 30	
GCC AAC ATC ACC ATT GTG GAG TCA AAC G	122
Ala Asn Ile Thr Ile Val Glu Ser Asn Ala	
35	

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

TCTAAACTA CAGAGACTGT ATTTTCATGA TCATCATAGT TCTGTGAAAT ATACTTAAAC	60
CGCTTTGGTC CTGATCTTGT AGG AAG TCA GAA CTT CGC ATT AGC AAA GCG	110
Lys Ser Glu Leu Arg Ile Ser Lys Ala	
1 5	
TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC AGC AAA CTA	158
Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu	
10 15 20 25	
GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG TCA AAC GGT	206
Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn Gly	
30 35 40	
AAG AGA TGC CTA CTG CGT GCT ATT TCT CAG TCT CTA AGA GGA GTG ATC	254
Lys Arg Cys Leu Leu Arg Ala Ile Ser Gln Ser Leu Arg Gly Val Ile	
45 50 55	
AAG GTA TGT GGT CAC ACT TGAATCACGC AGGTGTGTGA AATCTCATTG	302
Lys Val Cys Gly His Thr	
60	
TGAACAAATA AAAATCATGA AAGGAAACT CTATGTTTGA AATATCTTAT GGGTCCTCCT	362
GTAAAGCTCT TCACTCCATA AGGTGAAATA GACCTGAAAT ATATATAGAT TATTT	417

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

AG ATC ACC ACT GGC ATG CCA GCC TCA ACT GAG ACA GCG TAT GTG TCT	47
Glu Ile Thr Thr Gly Met Pro Ala Ser Thr Glu Thr Ala Tyr Val Ser	
1 5 10 15	
TCA GAG TCT CCC ATT AGA ATA TCA GTA TCA ACA GAA GGA ACA AAT ACT	95
Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Thr Asn Thr	
20 25 30	
TCT TCA T	102
Ser Ser Ser	
35	

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT GTG CCC 48
Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn Val Pro
1 5 10 15

ATG AAA GTC CAA ACC CAA GAA 69
Met Lys Val Gln Thr Gln Glu
20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG 48
Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met
1 5 10 15

GCC AGC TTC TAC 60
Ala Ser Phe Tyr
20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA TAG 36
Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

AAG CAT CTT GGG ATT GAA TTT ATG GAG
Lys His Leu Gly Ile Glu Phe Met Glu
1 5

27

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

AAA GCG GAG GAG CTC TAC CAG AAG AGA GTG CTC ACC ATT ACC GGC ATT
Lys Ala Glu Glu Leu Tyr Gln Lys Arg Val Leu Thr Ile Thr Gly Ile
1 5 10 15

48

TGC ATC GCG CTG CTC GTG GTT GGC ATC ATG TGT GTG GTG GTC TAC TGC
Cys Ile Ala Leu Leu Val Val Gly Ile Met Cys Val Val Val Tyr Cys
20 25 30

96

AAA ACC AAG AAA CAA CGG AAA AAG CTT CAT GAC CGG CTT CGG CAG AGC
Lys Thr Lys Lys Gln Arg Lys Lys Leu His Asp Arg Leu Arg Gln Ser
35 40 45

144

CTT CGG TCT GAA AGA AAC ACC ATG ATG AAC GTA GCC AAC GGG CCC CAC
Leu Arg Ser Glu Arg Asn Thr Met Met Asn Val Ala Asn Gly Pro His
50 55 60

192

CAC CCC AAT CCG CCC CCC GAG AAC GTG CAG CTG GTG AAT CAA TAC GTA
His Pro Asn Pro Pro Pro Glu Asn Val Gln Leu Val Asn Gln Tyr Val
65 70 75 80

240

TCT AAA AAT GTC ATC TCT AGC GAG CAT ATT GTT GAG AGA GAG GCG GAG
Ser Lys Asn Val Ile Ser Ser Glu His Ile Val Glu Arg Glu Ala Glu
85 90 95

288

AGC TCT TTT TCC ACC AGT CAC TAC ACT TCG ACA GCT CAT CAT TCC ACT
Ser Ser Phe Ser Thr Ser His Tyr Thr Ser Thr Ala His His Ser Thr
100 105 110

336

ACT	GTC	ACT	CAG	ACT	CCC	AGT	CAC	AGC	TGG	AGC	AAT	GGA	CAC	ACT	GAA	384
Thr	Val	Thr	Gln	Thr	Pro	Ser	His	Ser	Trp	Ser	Asn	Gly	His	Thr	Glu	
	115						120					125				
AGC	ATC	ATT	TCG	GAA	AGC	CAC	TCT	GTC	ATC	GTG	ATG	TCA	TCC	GTA	GAA	432
Ser	Ile	Ile	Ser	Glu	Ser	His	Ser	Val	Ile	Val	Met	Ser	Ser	Val	Glu	
	130					135					140					
AAC	AGT	AGG	CAC	AGC	AGC	CCG	ACT	GGG	GGC	CCG	AGA	GGA	CGT	CTC	AAT	480
Asn	Ser	Arg	His	Ser	Ser	Pro	Thr	Gly	Gly	Pro	Arg	Gly	Arg	Leu	Asn	
145					150					155					160	
GGC	TTG	GGA	GGC	CCT	CGT	GAA	TGT	AAC	AGC	TTC	CTC	AGG	CAT	GCC	AGA	528
Gly	Leu	Gly	Gly	Pro	Arg	Glu	Cys	Asn	Ser	Phe	Leu	Arg	His	Ala	Arg	
				165					170					175		
GAA	ACC	CCT	GAC	TCC	TAC	CGA	GAC	TCT	CCT	CAT	AGT	G	AAAG			569
Glu	Thr	Pro	Asp	Ser	Tyr	Arg	Asp	Ser	Pro	His	Ser					
		180						185								

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 730
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

G	TAT	GTA	TCA	GCA	ATG	ACC	ACC	CCG	GCT	CGT	ATG	TCA	CCT	GTA	GAT	46
	Tyr	Val	Ser	Ala	Met	Thr	Thr	Pro	Ala	Arg	Met	Ser	Pro	Val	Asp	
	1				5				10					15		
TTC	CAC	ACG	CCA	AGC	TCC	CCC	AAG	TCA	CCC	CCT	TCG	GAA	ATG	TCC	CCG	94
Phe	His	Thr	Pro	Ser	Ser	Pro	Lys	Ser	Pro	Pro	Ser	Glu	Met	Ser	Pro	
				20				25						30		
CCC	GTG	TCC	AGC	ACG	ACG	GTC	TCC	ATG	CCC	TCC	ATG	GCG	GTC	AGT	CCC	142
Pro	Val	Ser	Ser	Thr	Thr	Val	Ser	Met	Pro	Ser	Met	Ala	Val	Ser	Pro	
			35				40						45			
TTC	GTG	GAA	GAG	GAG	AGA	CCC	CTG	CTC	CTT	GTG	ACG	CCA	CCA	CGG	CTG	190
Phe	Val	Glu	Glu	Glu	Arg	Pro	Leu	Leu	Leu	Val	Thr	Pro	Pro	Arg	Leu	
		50					55					60				
CGG	GAG	AAG	TAT	GAC	CAC	CAC	GCC	CAG	CAA	TTC	AAC	TCG	TTC	CAC	TGC	238
Arg	Glu	Lys	Tyr	Asp	His	His	Ala	Gln	Gln	Phe	Asn	Ser	Phe	His	Cys	
	65					70					75					
AAC	CCC	GCG	CAT	GAG	AGC	AAC	AGC	CTG	CCC	CCC	AGC	CCC	TTG	AGG	ATA	286
Asn	Pro	Ala	His	Glu	Ser	Asn	Ser	Leu	Pro	Pro	Ser	Pro	Leu	Arg	Ile	
	80					85				90					95	

GTG GAG GAT GAG GAA TAT GAA ACG ACC CAG GAG TAC GAA CCA GCT CAA	334
Val Glu Asp Glu Glu Tyr Glu Thr Thr Gln Glu Tyr Glu Pro Ala Gln	
100 105 110	
GAG CCG GTT AAG AAA CTC ACC AAC AGC AGC CGG CGG GCC AAA AGA ACC	382
Glu Pro Val Lys Lys Leu Thr Asn Ser Ser Arg Arg Ala Lys Arg Thr	
115 120 125	
AAG CCC AAT GGT CAC ATT GCC CAC AGG TTG GAA ATG GAC AAC AAC ACA	430
Lys Pro Asn Gly His Ile Ala His Arg Leu Glu Met Asp Asn Asn Thr	
130 135 140	
GGC GCT GAC AGC AGT AAC TCA GAG AGC GAA ACA GAG GAT GAA AGA GTA	478
Gly Ala Asp Ser Ser Asn Ser Glu Ser Glu Thr Glu Asp Glu Arg Val	
145 150 155	
GGA GAA GAT ACG CCT TTC CTG GCC ATA CAG AAC CCC CTG GCA GCC AGT	526
Gly Glu Asp Thr Pro Phe Leu Ala Ile Gln Asn Pro Leu Ala Ala Ser	
160 165 170 175	
CTC GAG GCG GCC CCT GCC TTC CGC CTG GTC GAC AGC AGG ACT AAC CCA	574
Leu Glu Ala Ala Pro Ala Phe Arg Leu Val Asp Ser Arg Thr Asn Pro	
180 185 190	
ACA GGC GGC TTC TCT CCG CAG GAA GAA TTG CAG GCC AGG CTC TCC GGT	622
Thr Gly Gly Phe Ser Pro Gln Glu Glu Leu Gln Ala Arg Leu Ser Gly	
195 200 205	
GTA ATC GCT AAC CAA GAC CCT ATC GCT GTC TAAAACCGAA ATACACCCAT	672
Val Ile Ala Asn Gln Asp Pro Ile Ala Val	
210 215	
AGATTCACCT GTAAACTTT ATTTTATATA ATAAAGTATT CCACCTTAAA TTAAACAA	730

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1652
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

AGTTTCCCCC	CCCAACTTGT	CGGAACTCTG	GGCTCGCGCG	CAGGGCAGGA	GCGGAGCGGC	60
GGCGGCTGCC	CAGGCGATGC	GAGCGCGGGC	CGGACGGTAA	TCGCCTCTCC	CTCCTCGGGC	120
TGCGAGCGCG	CCGGACCGAG	GCAGCGACAG	GAGCGGACCG	CGGCGGGAAC	CGAGGACTCC	180
CCAGCGGCGC	GCCAGCAGGA	GCCACCCCGC	GAGCGTGCGA	CCGGGACGGA	GCGCCCGCCA	240
GTCCCAGGTG	GCCCGGACCG	CACGTTGCGT	CCCCGCGCTC	CCGCGCGGCG	ACAGGAGACG	300
CTCCCCCCCA	CGCCGCGCGC	GCCTCGGCCC	GGTCGCTGGC	CCGCCTCCAC	TCCGGGGACA	360
AACTTTTCCC	GAAGCCGATC	CCAGCCCTCG	GACCCAAACT	TGTCGCGCGT	CGCCTTCGCC	420
GGGAGCCGTC	CGCGCAGAGC	GTGCACTTCT	CGGGCGAG	ATG TCG GAG CGC AGA		473

Met Ser Glu Arg Arg
1 5

GAA	GGC	AAA	GGC	AAG	GGG	AAG	GGC	GGC	AAG	AAG	GAC	CGA	GGC	TCC	GGG	521
Glu	Gly	Lys	Gly	Lys	Gly	Lys	Gly	Gly	Lys	Lys	Asp	Arg	Gly	Ser	Gly	
				10					15					20		
AAG	AAG	CCC	GTG	CCC	GCG	GCT	GGC	GGC	CCG	AGC	CCA	GCC	TTG	CCT	CCC	569
Lys	Lys	Pro	Val	Pro	Ala	Ala	Gly	Gly	Pro	Ser	Pro	Ala	Leu	Pro	Pro	
				25					30					35		
CGC	TTG	AAA	GAG	ATG	AAG	ATG	CAG	GAG	TCT	GTG	GCA	GGT	TCC	AAA	CTA	617
Arg	Leu	Lys	Glu	Met	Lys	Ser	Gln	Glu	Ser	Val	Ala	Gly	Ser	Lys	Leu	
		40					45					50				
GTG	CTT	CGG	TGC	GAG	ACC	AGT	TCT	GAA	TAC	TCC	TCT	CTC	AAG	TTC	AAG	665
Val	Leu	Arg	Cys	Glu	Thr	Ser	Ser	Glu	Tyr	Ser	Ser	Leu	Lys	Phe	Lys	
	55					60						65				
TGG	TTC	AAG	AAT	GGG	AGT	GAA	TTA	AGC	CGA	AAG	AAC	AAA	CCA	CAA	AAC	713
Trp	Phe	Lys	Asn	Gly	Ser	Glu	Leu	Ser	Arg	Lys	Asn	Lys	Pro	Gln	Asn	
70					75					80					85	
ATC	AAG	ATA	CAG	AAA	AGG	CCG	GGG	AAG	TCA	GAA	CTT	CGC	ATT	AGC	AAA	761
Ile	Lys	Ile	Gln	Lys	Arg	Pro	Gly	Lys	Ser	Glu	Leu	Arg	Ile	Ser	Lys	
				90					95					100		
GCG	TCA	CTG	GCT	GAT	TCT	GGA	GAA	TAT	ATG	TGC	AAA	GTG	ATC	AGC	AAA	809
Ala	Ser	Leu	Ala	Asp	Ser	Gly	Glu	Tyr	Met	Cys	Lys	Val	Ile	Ser	Lys	
			105					110					115			
CTA	GGA	AAT	GAC	AGT	GCC	TCT	GCC	AAC	ATC	ACC	ATT	GTG	GAG	TCA	AAC	857
Leu	Gly	Asn	Asp	Ser	Ala	Ser	Ala	Asn	Ile	Thr	Ile	Val	Glu	Ser	Asn	
		120					125					130				
GAG	ATC	ACC	ACT	GGC	ATG	CCA	GCC	TCA	ACT	GAG	ACA	GCG	TAT	GTG	TCT	905
Glu	Ile	Thr	Thr	Gly	Met	Pro	Ala	Ser	Thr	Glu	Thr	Ala	Tyr	Val	Ser	
	135					140						145				
TCA	GAG	TCT	CCC	ATT	AGA	ATA	TCA	GTA	TCA	ACA	GAA	GGA	ACA	AAT	ACT	953
Ser	Glu	Ser	Pro	Ile	Arg	Ile	Ser	Val	Ser	Thr	Glu	Gly	Thr	Asn	Thr	
150					155					160					165	
TCT	TCA	TCC	ACA	TCC	ACA	TCT	ACA	GCT	GGG	ACA	AGC	CAT	CTT	GTC	AAG	1001
Ser	Ser	Ser	Thr	Ser	Thr	Ser	Thr	Ala	Gly	Thr	Ser	His	Leu	Val	Lys	
				170					175					180		
TGT	GCA	GAG	AAG	GAG	AAA	ACT	TTC	TGT	GTG	AAT	GGA	GGC	GAG	TGC	TTC	1049
Cys	Ala	Glu	Lys	Glu	Lys	Thr	Phe	Cys	Val	Asn	Gly	Gly	Glu	Cys	Phe	
			185					190					195			

ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC TTG TGC AAG TGC CCA	1097
Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys Pro	
200 205 210	
AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC	1145
Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe	
215 220 225	
TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA TAGGCGCATG	1193
Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu	
230 235 240	
CTCAGTCGGT GCCGCTTTCT TGTGCGCGCA TCTCCCCTCA GATTCAACCT AGAGCTAGAT	1253
GCGTTTTACC AGGTCTAACA TTGACTGCCT CTGCCTGTCG CATGAGAACA TTAACACAAG	1313
CGATTGTATG ACTTCCTCTG TCCGTGACTA GTGGGCTCTG AGCTACTCGT AGGTGCGTAA	1373
GGCTCCAGTG TTTCTGAAAT TGATCTTGAA TTACTGTGAT ACGACATGAT AGTCCCTCTC	1433
ACCCAGTGCA ATGACAATAA AGGCCTTGAA AAGTCTCACT TTTATTGAGA AAATAAAAAT	1493
CGTTCCACGG GACAGTCCCT CTTCTTTTATA AAATGACCCT ATCCTTGAAA AGGAGGTGTG	1553
TTAAGTTGTA ACCAGTACAC ACTTGAAATG ATGGTAAGTT CGCTTCGGTT CAGAATGTGT	1613
TCTTTCTGAC AAATAAACAG AATAAAAAAA AAAAAAAA A	1652

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1140
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

CAT CAN GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG	48
His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu	
1 5 10 15	
CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC TGC	96
Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys	
20 25 30	
GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG	144
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu	
35 40 45	
GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC CCC	192
Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro	
50 55 60	
TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG	240
Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val	
65 70 75 80	

[illegible]

CGTGACTAGT	GGGCTCTGAG	CTACTCGTAG	GTGCGTAAGG	CTCCAGTGTT	TCTGAAATTG	1050
ATCTTGAATT	ACTGTGATAC	GACATGATAG	TCCCTCTCAC	CCAGTGCAAT	GACAATAAAG	1110
GCCTTGAAAA	GTCAAAAAAA	AAAAAAAAAA				1140

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1764
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

G AAG TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA	49
Lys Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu	
1 5 10 15	
TAT ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC	97
Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala	
20 25 30	
AAC ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG	145
Asn Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly	
35 40 45	
ACA AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG	193
Thr Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val	
50 55 60	
AAT GGA GGC GAC TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA	241
Asn Gly Gly Asp Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg	
65 70 75 80	
TAC TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG	289
Tyr Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu	
85 90 95	
AAT GTG CCC ATG AAA GTC CAA ACC CAA GAA AAA GCG GAG GAG CTC TAC	337
Asn Val Pro Met Lys Val Gln Thr Gln Glu Lys Ala Glu Glu Leu Tyr	
100 105 110	
CAG AAG AGA GTG CTC ACC ATT ACC GGC ATT TGC ATC GCG CTG CTC GTG	385
Gln Lys Arg Val Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val	
115 120 125	
GTT GGC ATC ATG TGT GTG GTG GTC TAC TGC AAA ACC AAG AAA CAA CGG	433
Val Gly Ile Met Cys Val Val Val Tyr Cys Lys Thr Lys Lys Gln Arg	
130 135 140	

AAA Lys 145	AAG Lys	CTT Leu	CAT His	GAC Asp	CGG Arg 150	CTT Leu	CGG Arg	CAG Gln	AGC Ser	CTT Leu 155	CGG Arg	TCT Ser	GAA Glu	AGA Arg	AAC Asn 160	481
ACC Thr	ATG Met	ATG Met	AAC Asn	GTA Val 165	GCC Ala	AAC Asn	GGG Gly	CCC Pro	CAC His 170	CAC His	CCC Pro	AAT Asn	CCG Pro	CCC Pro 175	CCC Pro	529
GAG Glu	AAC Asn	GTG Val	CAG Gln 180	CTG Leu	GTG Val	AAT Asn	CAA Gln 185	TAC Tyr	GTA Val	TCT Ser	AAA Lys	AAT Asn	GTC Val 190	ATC Ile	TCT Ser	577
AGC Ser	GAG Glu	CAT His 195	ATT Ile	GTT Val	GAG Glu	AGA Arg	GAG Glu 200	GCG Ala	GAG Glu	AGC Ser	TCT Ser	TTT Phe 205	TCC Ser	ACC Thr	AGT Ser	625
CAC His	TAC Tyr 210	ACT Thr	TCG Ser	ACA Thr	GCT Ala	CAT His 215	CAT His	TCC Ser	ACT Thr	ACT Thr	GTC Val 220	ACT Thr	CAG Gln	ACT Thr	CCC Pro	673
AGT Ser 225	CAC His	AGC Ser	TGG Trp	AGC Ser	AAT Asn 230	GGA Gly	CAC His	ACT Thr	GAA Glu	AGC Ser 235	ATC Ile	ATT Ile	TCG Ser	GAA Glu	AGC Ser 240	721
CAC His	TCT Ser	GTC Val	ATC Ile	GTG Val 245	ATG Met	TCA Ser	TCC Ser	GTA Val	GAA Glu 250	AAC Asn	AGT Ser	AGG Arg	CAC His	AGC Ser 255	AGC Ser	769
CCG Pro	ACT Thr	GGG Gly	GGC Gly 260	CCG Pro	AGA Arg	GGA Gly	CGT Arg	CTC Leu 265	AAT Asn	GGC Gly	TTG Leu	GGA Gly	GGC Gly 270	CCT Pro	CGT Arg	817
GAA Glu	TGT Cys	AAC Asn 275	AGC Ser	TTC Phe	CTC Leu	AGG Arg	CAT His 280	GCC Ala	AGA Arg	GAA Glu	ACC Thr	CCT Pro 285	GAC Asp	TCC Ser	TAC Tyr	865
CGA Arg 290	GAC Asp	TCT Ser	CCT Pro	CAT His	AGT Ser	GAA Glu 295	AGA Arg	CAT His	AAC Asn	CTT Leu 300	ATA Ile	GCT Ala	GAG Glu	CTA Leu	AGG Arg	913
AGA Arg 305	AAC Asn	AAG Lys	GCC Ala	CAC His	AGA Arg 310	TCC Ser	AAA Lys	TGC Cys	ATG Met	CAG Gln 315	ATC Ile	CAG Gln	CTT Leu	TCC Ser	GCA Ala 320	961
ACT Thr	CAT His	CTT Leu	AGA Arg	GCT Ala 325	TCT Ser	TCC Ser	ATT Ile	CCC Pro	CAT His 330	TGG Trp	GCT Ala	TCA Ser	TTC Phe	TCT Ser 335	AAG Lys	1009
ACC Thr	CCT Pro	TGG Trp	CCT Pro 340	TTA Leu	GGA Gly	AGG Arg	TAT Tyr	GTA Val 345	TCA Ser	GCA Ala	ATG Met	ACC Thr	ACC Thr	CCG Pro 350	GCT Ala	1057

[illegible]

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys
1 5 10 15
Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys
20 25 30
Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser
35 40 45
Phe Tyr
50

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys
1 5 10 15
Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys
20 25 30
Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn Val Pro Met Lys
35 40 45
Val Gln
50

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

Glu Cys Leu Arg Lys Tyr Lys Asp Phe Cys Ile His Gly Glu Cys Lys
1 5 10 15
Tyr Val Lys Glu Leu Arg Ala Pro Ser Cys Lys Cys Gln Gln Glu Tyr
20 25 30
Phe Gly Glu Arg Cys Gly Glu Lys Ser Asn Lys Thr His Ser
35 40 45

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1 5 10 15
GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
20 25 30
TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC 144
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr
35 40 45
GTA ATG GCC AGC TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT 192
Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro
50 55 60
GAA TAG 198
Glu
65

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

AGC	CAT	CTT	GTC	AAG	TGT	GCA	GAG	AAG	GAG	AAA	ACT	TTC	TGT	GTG	AAT	48
Ser	His	Leu	Val	Lys	Cys	Ala	Glu	Lys	Glu	Lys	Thr	Phe	Cys	Val	Asn	
1				5					10					15		
GGA	GGC	GAG	TGC	TTC	ATG	GTG	AAA	GAC	CTT	TCA	AAT	CCC	TCA	AGA	TAC	96
Gly	Gly	Glu	Cys	Phe	Met	Val	Lys	Asp	Leu	Ser	Asn	Pro	Ser	Arg	Tyr	
			20					25					30			
TTG	TGC	AAG	TGC	CAA	CCT	GGA	TTC	ACT	GGA	GCG	AGA	TGT	ACT	GAG	AAT	144
Leu	Cys	Lys	Cys	Gln	Pro	Gly	Phe	Thr	Gly	Ala	Arg	Cys	Thr	Glu	Asn	
		35					40					45				
GTG	CCC	ATG	AAA	GTC	CAA	ACC	CAA	GAA	AAA	GCG	GAG	GAG	CTC	TAC	TAA	192
Val	Pro	Met	Lys	Val	Gln	Thr	Gln	Glu	Lys	Ala	Glu	Glu	Leu	Tyr		
	50					55					60					

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

AGC	CAT	CTT	GTC	AAG	TGT	GCA	GAG	AAG	GAG	AAA	ACT	TTC	TGT	GTG	AAT	48
Ser	His	Leu	Val	Lys	Cys	Ala	Glu	Lys	Glu	Lys	Thr	Phe	Cys	Val	Asn	
1				5					10					15		
GGA	GGC	GAG	TGC	TTC	ATG	GTG	AAA	GAC	CTT	TCA	AAT	CCC	TCA	AGA	TAC	96
Gly	Gly	Glu	Cys	Phe	Met	Val	Lys	Asp	Leu	Ser	Asn	Pro	Ser	Arg	Tyr	
			20					25					30			
TTG	TGC	AAG	TGC	CCA	AAT	GAG	TTT	ACT	GGT	GAT	CGC	TGC	CAA	AAC	TAC	144
Leu	Cys	Lys	Cys	Pro	Asn	Glu	Phe	Thr	Gly	Asp	Arg	Cys	Gln	Asn	Tyr	
		35					40					45				
GTA	ATG	GCC	AGC	TTC	TAC	AAA	GCG	GAG	GAG	CTC	TAC	TAA				183
Val	Met	Ala	Ser	Phe	Tyr	Lys	Ala	Glu	Glu	Leu	Tyr					
	50					55				60						

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT	48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn	
1 5 10 15	
GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC	96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr	
20 25 30	
TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC	144
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr	
35 40 45	
GTA ATG GCC AGC TTC TAC AAG CAT CTT GGG ATT GAA TTT ATG GAG AAA	192
Val Met Ala Ser Phe Tyr Lys His Leu Gly Ile Glu Phe Met Glu Lys	
50 55 60	
GCG GAG GAG CTC TAC TAA	210
Ala Glu Glu Leu Tyr	
65	

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT	48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn	
1 5 10 15	
GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC	96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr	
20 25 30	
TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT	144
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn	
35 40 45	
GTG CCC ATG AAA GTC CAA ACC CAA GAA AAG TGC CCA AAT GAG TTT ACT	192

Val Pro Met Lys Val Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr
50 55 60

GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AGT ACG TCC 240
Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser
65 70 75 80

ACT CCC TTT CTG TCT CTG CCT GAA TAG 267
Thr Pro Phe Leu Ser Leu Pro Glu
85

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1 5 10 15

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
20 25 30

TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT 144
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn
35 40 45

GTG CCC ATG AAA GTC CAA ACC CAA GAA AAG TGC CCA AAT GAG TTT ACT 192
Val Pro Met Lys Val Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr
50 55 60

GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AAA GCG GAG 240
Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Lys Ala Glu
65 70 75 80

GAG CTC TAC TAA 252
Glu Leu Tyr

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

CC ACA TCC ACA TCT ACA GCT GGG ACA AGC CAT CTT GTC AAG TGT GCA	47
Thr Ser Thr Ser Thr Ala Gly Thr Ser His Leu Val Lys Cys Ala	
1 5 10 15	
GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGC GAG TGC TTC ATG GTG	95
Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys Phe Met Val	
20 25 30	
AAA GAC CTT TCA AAT CCC TCA AGA TAC TTG T GC	128
Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu	
35 40	

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

A CAT AAC CTT ATA GCT GAG CTA AGG AGA AAC AAG GCC CAC AGA TCC	46
His Asn Leu Ile Ala Glu Leu Arg Arg Asn Lys Ala His Arg Ser	
1 5 10 15	
AAA TGC ATG CAG ATC CAG CTT TCC GCA ACT CAT CTT AGA GCT TCT TCC	94
Lys Cys Met Gln Ile Gln Leu Ser Ala Thr His Leu Arg Ala Ser Ser	
20 25 30	
ATT CCC CAT TGG GCT TCA TTC TCT AAG ACC CCT TGG CCT TTA GGA AG	141
Ile Pro His Trp Ala Ser Phe Ser Lys Thr Pro Trp Pro Leu Gly Arg	
35 40 45	

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in positions 15 and 22 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

Ala Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Xaa Phe
1 5 10 15

Met Val Lys Asp Leu Xaa Asn Pro
20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 745
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

ATG AGA TGG CGA CGC GCC CCG CGC CGC TCC GGG CGT CCC GGC CCC CGG 48
Met Arg Trp Arg Arg Ala Pro Arg Arg Ser Gly Arg Pro Gly Pro Arg
1 5 10 15

GCC CAG CGC CCC GGC TCC GCC GCC CGC TCG TCG CCG CCG CTG CCG CTG 96
Ala Gln Arg Pro Gly Ser Ala Ala Arg Ser Ser Pro Pro Leu Pro Leu
20 25 30

CTG CCA CTA CTG CTG CTG CTG GGG ACC GCG GCC CTG GCG CCG GGG GCG 144
Leu Pro Leu Leu Leu Leu Leu Gly Thr Ala Ala Leu Ala Pro Gly Ala
35 40 45

GCG GCC GGC AAC GAG GCG GCT CCC GCG GGG GCC TCG GTG TGC TAC TCG 192
Ala Ala Gly Asn Glu Ala Ala Pro Ala Gly Ala Ser Val Cys Tyr Ser
50 55 60

TCC CCG CCC AGC GTG GGA TCG GTG CAG GAG CTA GCT CAG CGC GCC GCG 240
Ser Pro Pro Ser Val Gly Ser Val Gln Glu Leu Ala Gln Arg Ala Ala
65 70 75 80

GTG GTG ATC GAG GGA AAG GTG CAC CCG CAG CGG CGG CAG CAG GGG GCA 288
Val Val Ile Glu Gly Lys Val His Pro Gln Arg Arg Gln Gln Gly Ala
85 90 95

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 167:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) **FEATURE:**

(D) OTHER INFORMATION: N in positions 25 and 36 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

ATAGGGAAGG GCGGGGGAAG GGTCNCCCTC NGCAGGGCCG GGCTTGCCTC TGGAGCCTCT

60

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 168:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) **FEATURE:**

(D) OTHER INFORMATION: N in position 16 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

TTTACACATA TATTCNCC 18

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

Glu Thr Gln Pro Asp Pro Gly Gln Ile Leu Lys Lys Val Pro Met Val
1 5 10 15

Ile Gly Ala Tyr Thr
20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

Met	Arg	Trp	Arg	Arg	Ala	Pro	Arg	Arg	Ser	Gly	Arg	Pro	Gly	Pro	Arg	
1					5				10					15		
Ala	Gln	Arg	Pro	Gly	Ser	Ala	Ala	Arg	Ser	Ser	Pro	Pro	Leu	Pro	Leu	
			20					25					30			
Leu	Pro	Leu	Leu	Leu	Leu	Leu	Gly	Thr	Ala	Ala	Leu	Ala	Pro	Gly	Ala	
		35					40					45				
Ala	Ala	Gly	Asn	Glu	Ala	Ala	Pro	Ala	Gly	Ala	Ser	Val	Cys	Tyr	Ser	
	50					55					60					
Ser	Pro	Pro	Ser	Val	Gly	Ser	Val	Gln	Glu	Leu	Ala	Gln	Arg	Ala	Ala	
65					70					75					80	
Val	Val	Ile	Glu	Gly	Lys	Val	His	Pro	Gln	Arg	Arg	Gln	Gln	Gly	Ala	
				85					90					95		
Leu	Asp	Arg	Lys	Ala	Ala	Ala	Ala	Ala	Gly	Glu	Ala	Gly	Ala	Trp	Gly	
			100					105					110			
Gly	Asp	Arg	Glu	Pro	Pro	Ala	Ala	Gly	Pro	Arg	Ala	Leu	Gly	Pro	Pro	
		115					120					125				
Ala	Glu	Glu	Pro	Leu	Leu	Ala	Ala	Asn	Gly	Thr	Val	Pro	Ser	Trp	Pro	
	130					135					140					
Thr	Ala	Pro	Val	Pro	Ser	Ala	Gly	Glu	Pro	Gly	Glu	Glu	Ala	Pro	Tyr	
145					150					155					160	
Leu	Val	Lys	Val	His	Gln	Val	Trp	Ala	Val	Lys	Ala	Gly	Gly	Leu	Lys	
				165					170					175		
Lys	Asp	Ser	Leu	Leu	Thr	Val	Arg	Leu	Gly	Thr	Trp	Gly	His	Pro	Ala	
			180					185					190			
Phe	Pro	Ser	Cys	Gly	Arg	Leu	Lys	Glu	Asp	Ser	Arg	Tyr	Ile	Phe	Phe	
		195					200					205				
Met	Glu	Pro	Asp	Ala	Asn	Ser	Thr	Ser	Arg	Ala	Pro	Ala	Ala	Phe	Arg	
	210					215					220					
Ala	Ser	Phe	Pro	Pro	Leu	Glu	Thr	Gly	Arg	Asn	Leu	Lys	Lys	Glu	Val	
225					230					235					240	

Pro Arg Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu Gly Ala Tyr
 35 40 45

Val Ser Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Ala
 50 55 60

Asn Thr Ser Ser Ser
 65

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 172:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

Arg Lys Gly Asp Val Pro Gly Pro Arg Val Lys Ser Ser Arg Ser Thr
 1 5 10 15

Thr Thr Ala

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 173:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

CGCGAGCGCC	TCAGCGCGGC	CGCTCGCTCT	CCCCCTCGAG	GGACAAACTT	TTCCCAAACC	60
CGATCCGAGC	CCTTGGACCA	AACTCGCCTG	CGCCGAGAGC	CGTCCGCGTA	GAGCGCTCCG	120
TCTCCGGCGA	GATGTCCGAG	CGCAAAGAAG	GCAGAGGCAA	AGGGAAGGGC	AAGAAGAAGG	180
AGCGAGGCTC	CGGCAAGAAG	CCGGAGTCCG	CGGCGGGCAG	CCAGAGCCCA	G	231

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

CCTTGCCTCC	CCGATTGAAA	GAGATGAAAA	GCCAGGAATC	GGCTGCAGGT	TCCAAACTAG	60
TCCTTCGGTG	TGAAACCAGT	TCTGAATACT	CCTCTCTCAG	ATTCAAGTGG	TTCAAGAATG	120
GGAATGAATT	GAATCGAAAA	AACAAACCAC	AAAATATCAA	GATACAAAAA	AAGCCAGG	178

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

GAAGTCAGAA	CTTCGCATTA	ACAAAGCATC	ACTGGCTGAT	TCTGGAGAGT	ATATGTGCAA	60
AGTGATCAGC	AAATTAGGAA	ATGACAGTGC	CTCTGCCAAT	ATCACCATCG	TGGAATCAAA	120
CG						122

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

AGATCATCAC	TGGTATGCCA	GCCTCAACTG	AAGGAGCATA	TGTGTCTTCA	GAGTCTCCCA	60
TTAGAATATC	AGTATCCACA	GAAAGGAGCAA	ATACTTCTTC	AT		102

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

CTACATCTAC ATCCACCACT GGGACAAGCC ATCTTGTAAG ATGTGCGGAG AAGGAGAAAA	60
CTTTCTGTGT GAATGGAGGG GAGTGCTTCA TGGTGAAAGA CCTTTCAAAC CCCTCGAGAT	120
ACTTGTGC	128

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

AAGTGCCAAC CTGGATTCAC TGGAGCAAGA TGTACTGAGA ATGTGCCCAT GAAAGTCCAA	60
AACCAAGAA	69

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

TCGGGCTCCA TGAAGAAGAT GTA	23
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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

TCCATGAAGA AGATGTACCT GCT	23
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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 181

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

ATGTACCTGC TGTCTCCTT GA

22

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 182

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

TTGAAGAAGG ACTCGCTGCT CA

22

C' cont
(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 183

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

AAAGCCGGGG GCTTGAAGAA

20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 184

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

ATGARGTGTG GGCGGCGAAA

20